

## FIGURE 1A

[illegible]

—

FIGURE 1C

[illegible]

Comparison of human (HUM) and mouse (MUS) stauken sequences

			→ RBD1	
HUM	MKLGKKPMYKFPVDPYSRMQSTYNYNMRGGAYPPRYFYFPFVPPILLYQVELSVGGQQFNGK	60		
	.....			
MUS	MYKFPVDPHSRMQSTYSYGMRGGAYPPRYFYFPFVPPILLYQVELSVGGQQFNGK			
	RBD1←		→ RBD2	
HUM	GKTRQAAKHDAAAKALRILQNEPLPERLEVNGRESEEEENLNKSEISQVFEIALKRNLPVN	120		
	:: .....			
MUS	GKMRPPVKHDAPARALRTLQSEPLPERLEVNGREAEEENLNKSEISQVFEIALKRNLPVN			
			RBD2←	
HUM	FEVARESGLPHMKNFVTKVSVGEFVGE GEGSKKISKKNAAIAVLEELKKLPPLPAVERV	180		
	.....			
MUS	FEVARESGLPHMKNFVTRVSVGEFVGE GEGSKKISKKNAAIAVLEELRRLPPLPAVERV			
			→ RBD3	
HUM	KPRIKKKTKPIVKPQTSPEYQGGINPISRLAQIQAKKEKEPEYTLTTERGLPRRREFVM	240		
	.....			
MUS	KPRIKKKSQPTCK--TAPDYQGMNPISRLAQIQAKKEKEPEYMLLTERGLPRRREFVM			
	RBD3←		→ TED	
HUM	QVKVGNHTAEGTGTNKKVAKRNAAENMLEILGFKVPQRQPTKPALKSEEKTPIKKPGDGR	300		
	.....			
MUS	QVKVGHHTAEGVGTNKKVAKRNAAENMLEILGFKVPQAQPAKPAKSEEKTPVKKPGDGR			
HUM	KVTFFDPGSGDENGTSNKEDEFRMPYLSHQQLPAGILPMVPEVAQAVGVSQGHHTKDFTR	360		
	.....			
MUS	KVTFFEPSPGDENGTSNKEDEFRMPYLSHQQLPAGILPMVPEVAQAVGVSQGHHTKDFTR			
			TED←	
HUM	AAPNPAKATVTAMIARELLYGGTSPTAETILKNNISSGHVPHGPLTRPSEQLDYLSRVQG	420		
	.....			
MUS	AAPNPAKATVTAMIARELLYGGTSPTAETILKSNISSGHVPHGPRTRPSEQLYYLSRAQG			
			→ RBD4	RBD4←
HUM	FQVEYKDFPKNNKNEFVSLINCSSQPPLISHGIGKDVESCHDMAALNILKLLSELDQQST	480		
	.....			
MUS	FQVEYKDFPKNNKNECVSLINCSSQPPLVSHGIGKDVESCHDMAALNILKLLSELDQQST			
HUM	EMPRTGNGPMSVCGRC*	496		
	.....			
MUS	EMPRTGNGPVSACGTC*			

FIGURE 1D



```

698      >RBD4<
DRO ppkklldmddadnpitkllqlqqrkekepefeliakngnetarrrefvmeaasgstartgtgnkklakrnaaqalfelleavqvtpntnetqsseecccteatmsavtapaveataegk
HUM -----GGINPISRLAQIQOAKKEPEYITLLTERGLP--RRREFVMQVKVGNHTAEGTGNKVKAKRNAANALEILGFKVPOQPTKQALKSEKTPIKKPGDGGRKVTFFOPGS
CEL -----ghqinpvslivqtqakekehtfelvaehgve--kykefiiqkvvgddvqegkgnkrlakraaeamlesigfvtkpippgkellkkmldodpelpelshwtgppptav
C      PI V E K P F V GP H K F F V VG G G SKK AK AA AL L
      L R Y L R M

```

```

818
DRO vpmvactpvgtppgilllrqnkkpkakkrdrqivivkenvekeeeankevavaseenennneanngdsesngdsqataaeesalntstqstntsgvssnsnvgantdgnnhaesknntes
HUM GDENGTSNKEDFRMP-----YLSHQQLPAGILPMVPEVAQVGSQCHHTKDFTRAAPNP-AKATVTAMJARELLYGGTSP---TAETILKNN-----ISSGHVPHGPLTRPS---
CEL svsteepdtseaaqlspeqtdisekrelelepdtekrvrtfnagvhacpppgddypnsivqslkkdaivegkrrlrkrakenrralttaeqivelseeraqsy/qtknttiqesqessah---
C

```

```

938      >RBD5<
DRO eenstantqsagvhmkeqllylskllldfevnfsdypkgnhnefltivtlsthppqichgvvgkseeesqndaaenalkilekiglnnamk*
HUM -----EQLDYLSRVQGFQVEYKQFPKNKNEFVSLINCSQPLISHGIGKOVESCHDMAALNIIKLSELQOOSTENMPRTGNGPMVSGRC*
CEL -----hhleqlsdrfxfsalqytsfpqvgidqhtivaiglesplvghgtgcstteadensaldaiaklkelesakt*
C      G G SKK AK AA AL L

```

B)

```

230      STAU FEN      GFKVPQROPTKPAKSEKTPIKKPGDGGRKVTTFDPGSGDENGTSNKEDFELPYLSHQQLPAGILPMVPEVAQVGSQCHHTKDFTRAAPNPAKATVTA      323
247      MAP1B      KEKTKTKGPGTKTKS88PVKSDGKSKPLAASPKPAGLKESSDKVSRVASPKKGSVEKAAKPTTTPEVKAARGEENDKE TKNAANASASKSAKTATA      2337

```

FIGURE 1' (cont'd)

c)

FIGURE 1' (cont'd)

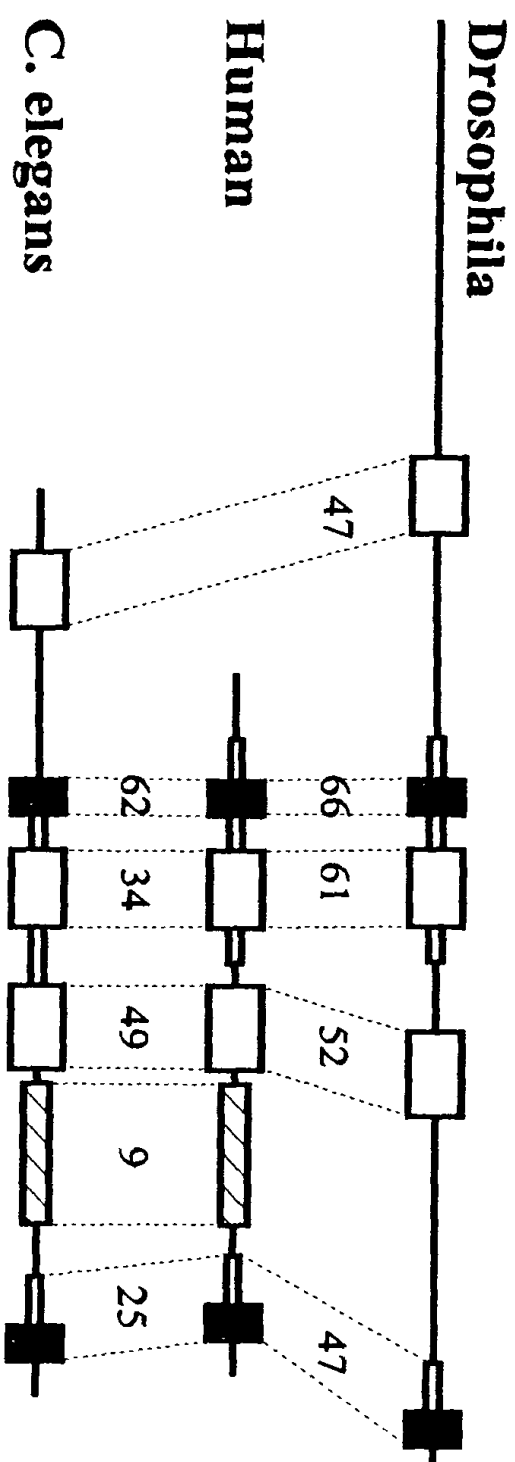


FIGURE 2

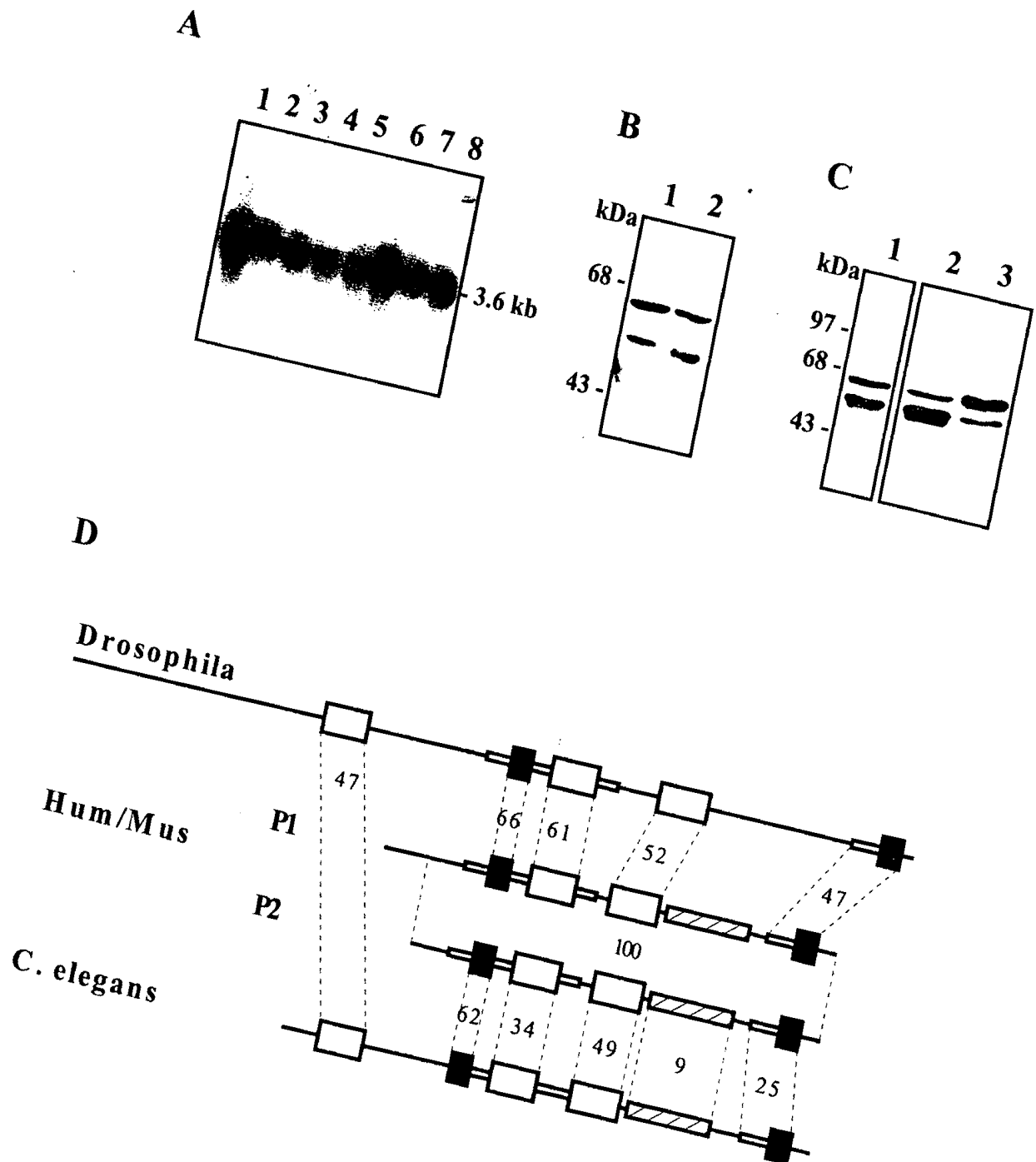
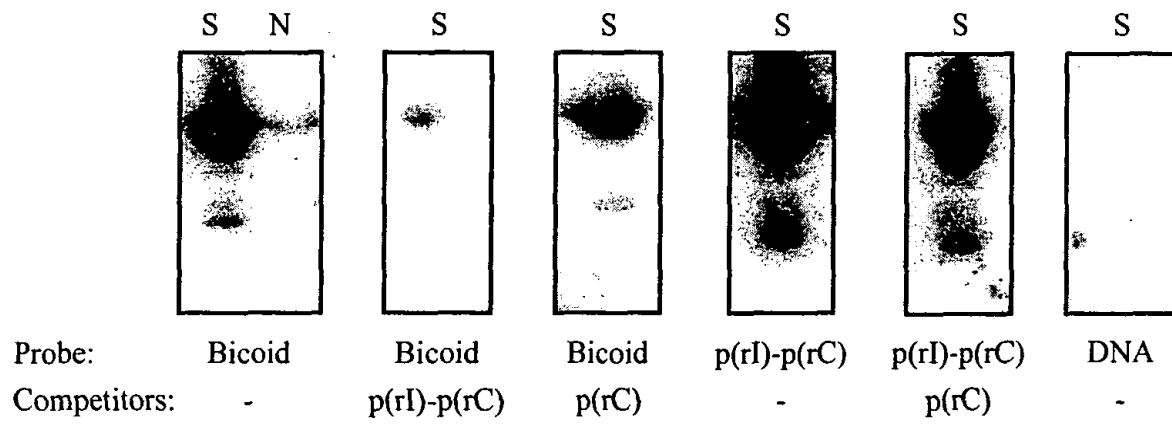




FIGURE 3

A



B

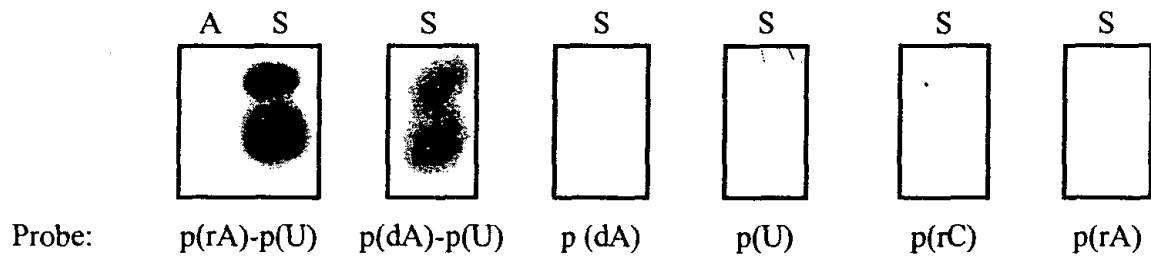


FIGURE 4

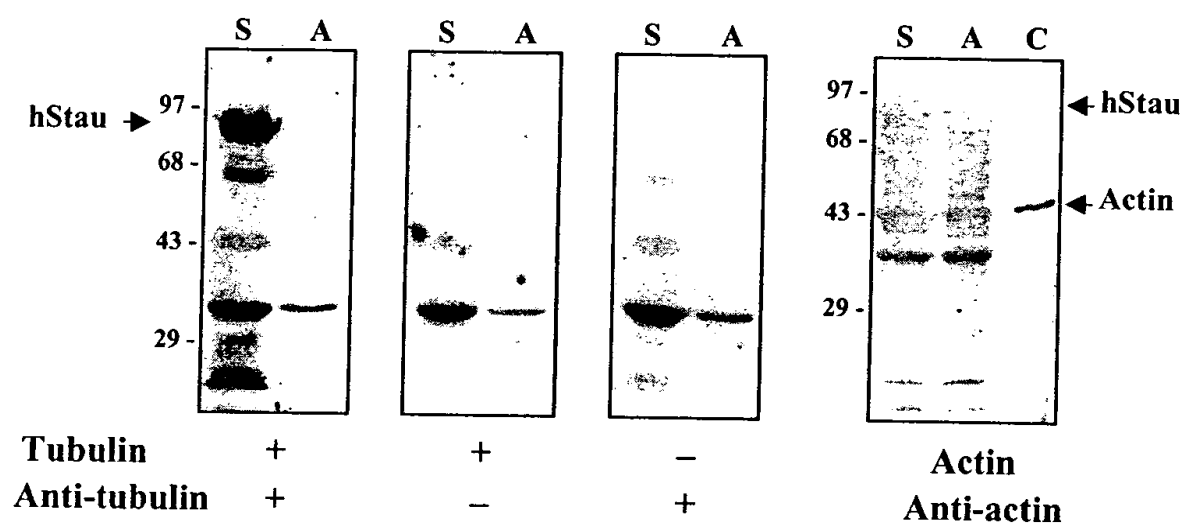
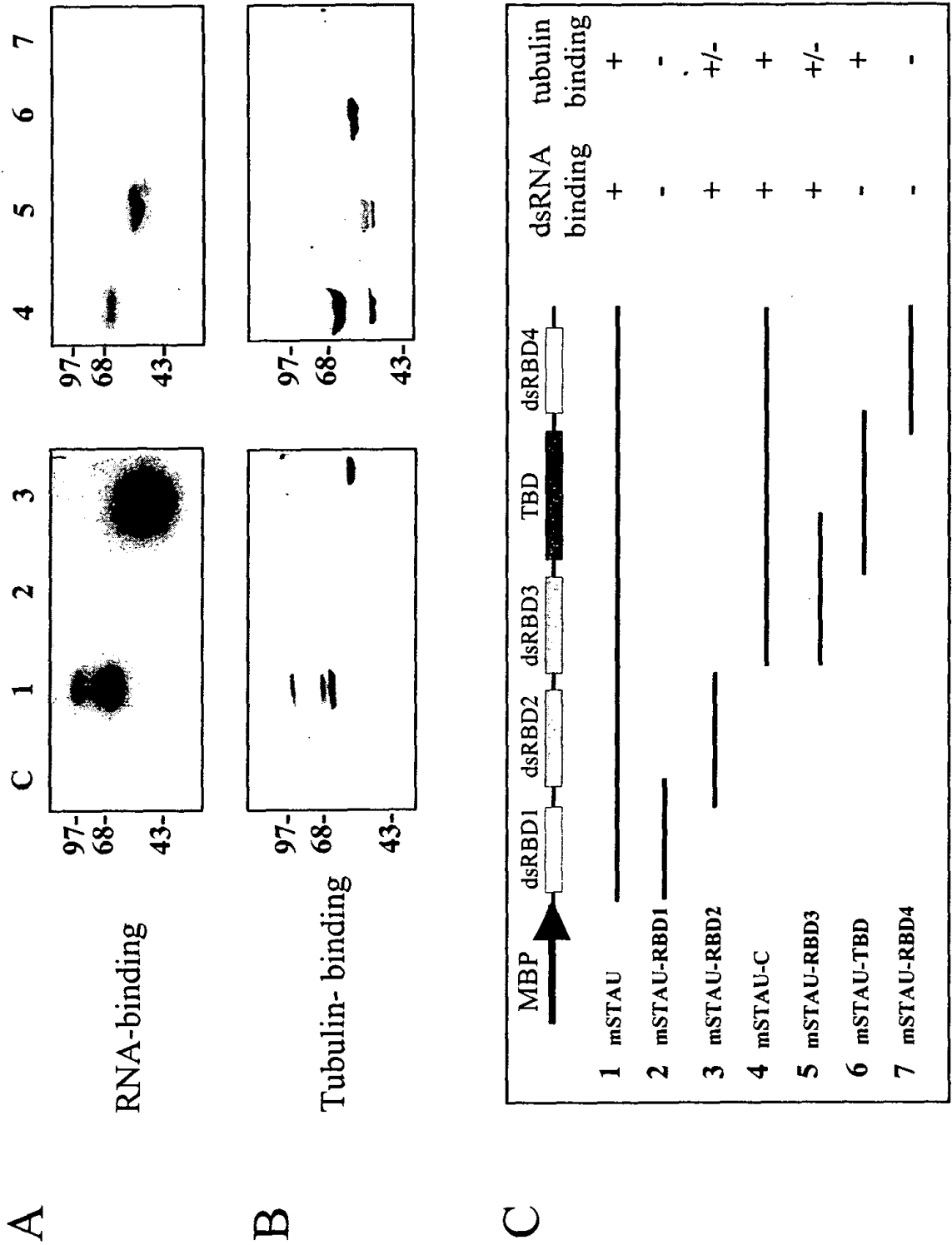


FIGURE 5



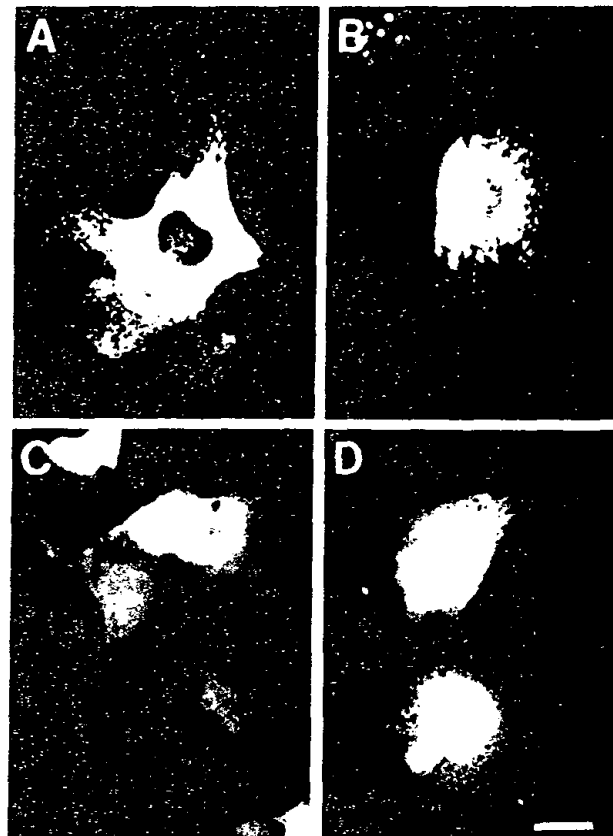


FIGURE 6

FIGURE 7

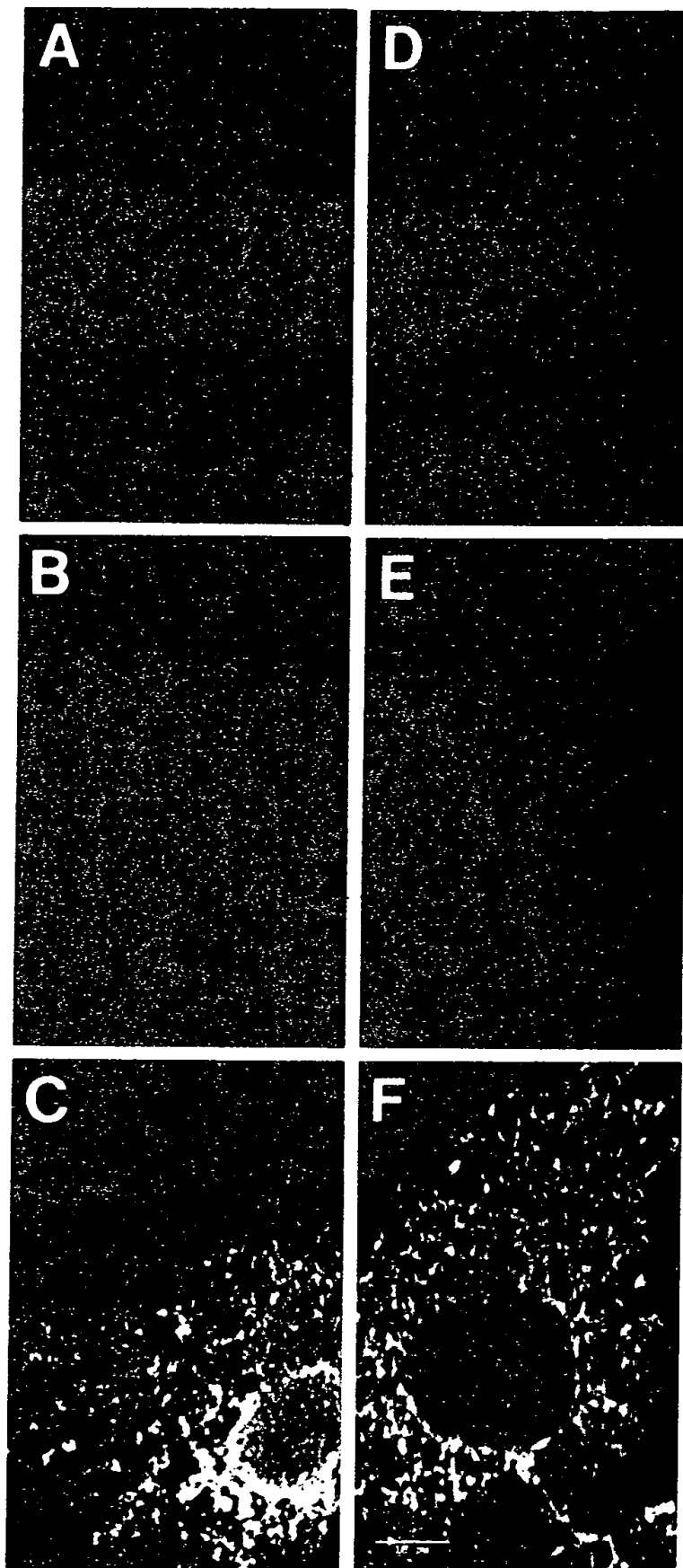
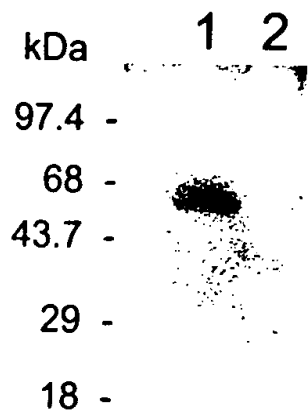
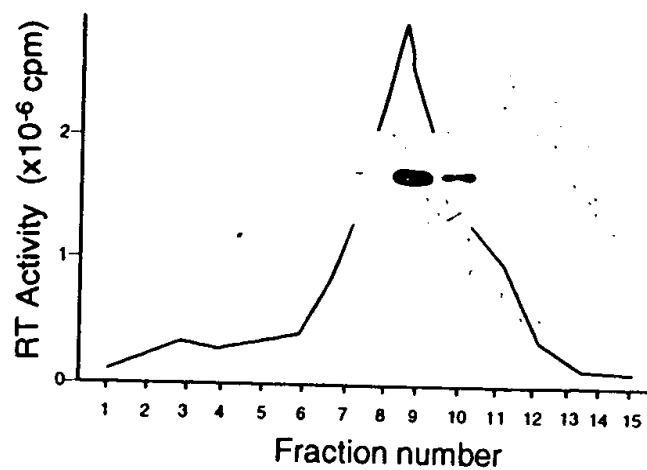


FIGURE 8

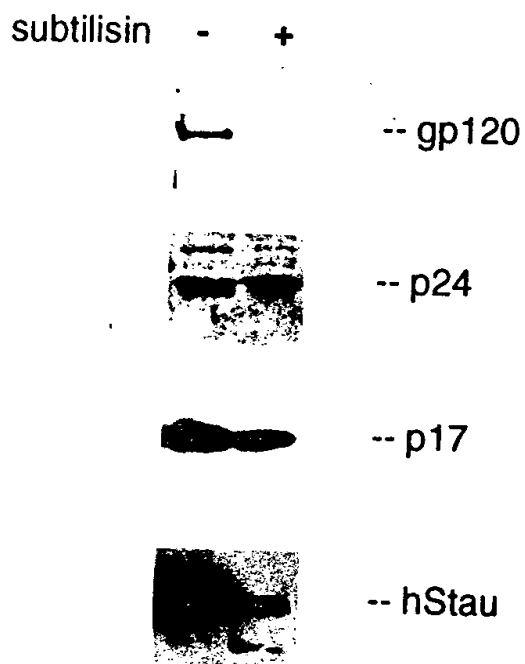
A



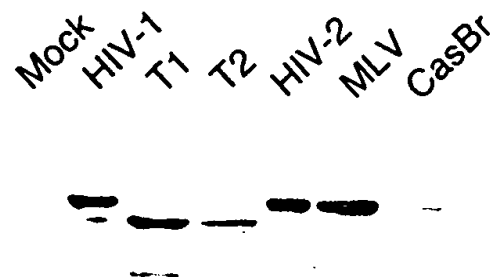
B



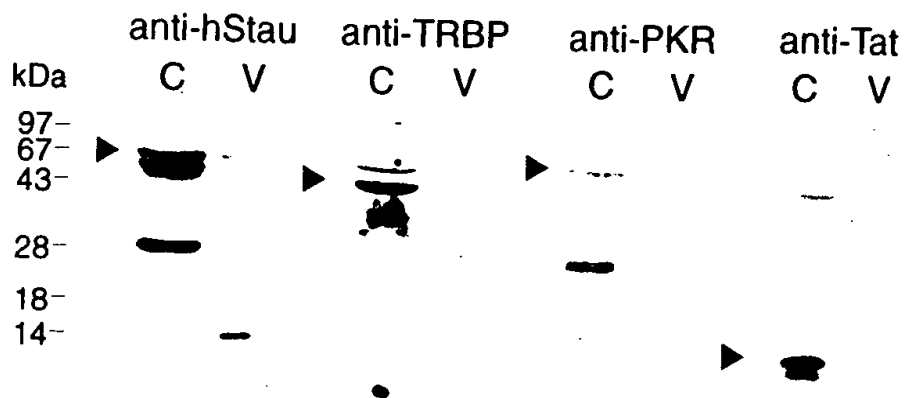
C



D



E



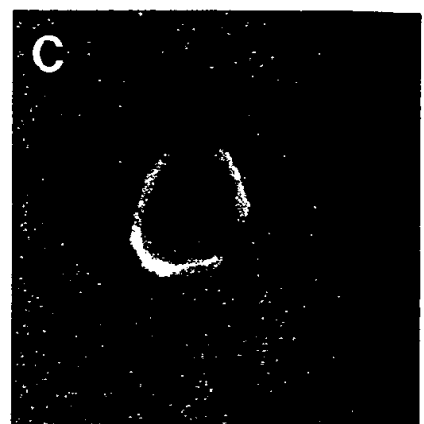
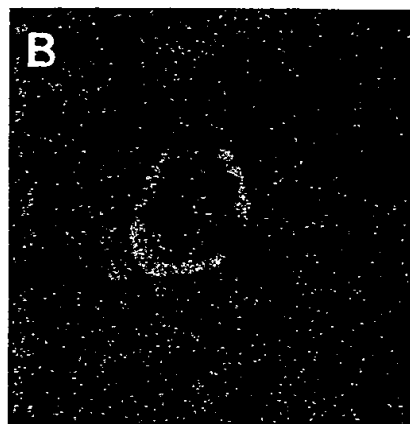
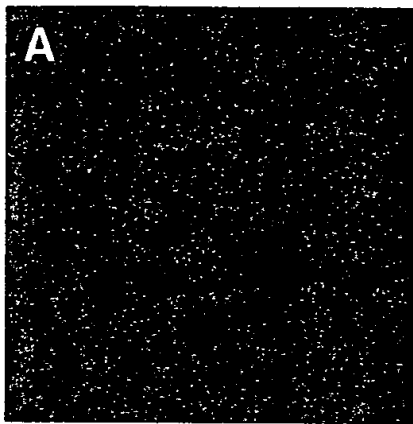


FIGURE 9

FIGURE 10

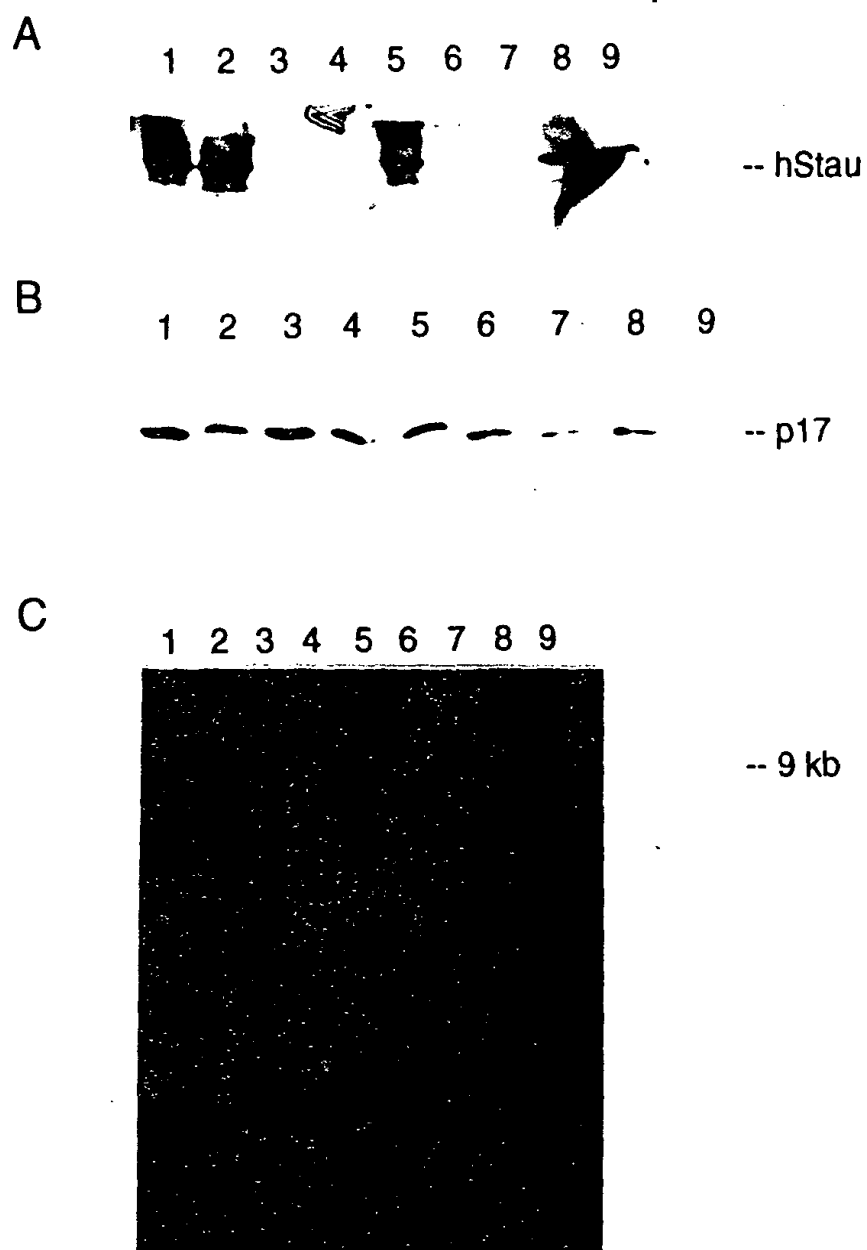




FIGURE 11

